REMARKS

Claims 1-30 are presently pending in the application. Claims 15, 20-23 and 25 have been withdrawn from consideration pursuant to a restriction requirement that has been made FINAL. Applicants reserve the right to file a continuing application directed to the subject matter of the withdrawn claims at any time during the pendency of this application. Examined claims 1-14, 16-19, 24, and 26-30 stand variously rejected under 35 U.S.C. §§ 102/103.

Specification

The disclosure was objected to because an application was referenced by a docket number rather than application number. The foregoing amendment to the specification obviates this objection.

Information Disclosure Statement

Applicants thank Examiner Brusca for considering the Strausberg and IHGSC publications and for listing these references on PTO Form 892.

Rejections Under 35 U.S.C. § 102(b)

Claims 1, 2, 4-12, 18, 19 and 24 stand rejected as allegedly anticipated under 35 U.S.C. § 102(b) by Liu et al. (1997) PNAS (hereinafter "Liu"). In support of this rejection, Liu is cited as follows:

> Liu et al. show on pages 5528-5529 and figure 4 modulation of expression of a target luciferase gene in a human cultured HeLa cell by introduction of an expression vector that expresses a zinc finger protein linked alternatively to a VP16 activation domain or a Krab-A repression domain. The phenotype measured was expression at the protein level of the luciferase gene product, which inherently also measures transcription of the luciferase gene. The zinc finger protein binds to a site in the promoter region of the luciferase gene (see page 5526). Liu et al. discusses the use of zinc finger proteins to modulate gene expression by binding within the coding region in the first column of page 5529. (Office Action, paragraph 7, page 4).

Because Liu fails to describe, demonstrate or suggest methods of identifying a gene as set forth in the body of the pending claims, Applicants traverse the rejection and supporting remarks.

None of the claims at issue are directed to methods of modulating gene expression of a predetermined gene as described in Liu. Rather, the claims recite methods of identifying putative gene sequences. As set forth in the body of claim 1, putative gene sequences (PGS) are identified as gene (or non-gene) by providing a cell comprising the PGS and then assaying the

ability of an exogenous molecule that binds to and/or modulates expression of the PGS to change the phenotype of the cell. The Office has ignored step (a) of independent claim 1, which requires that a putative gene sequence be obtained. Nowhere does Liu describe or suggest obtaining a putative gene sequence. Liu relates entirely to methods modulating expression of a known gene. There is nothing in Liu that teaches how to identify whether or not a particular sequence is part of a gene.

Thus, since Liu does not describe or demonstrate each and every step of the claimed methods, this reference cannot anticipate the pending claims and Applicants respectfully request that this rejection be withdrawn.

Rejections Under 35 U.S.C. § 103

Claims 1, 3, 13, 14, 16, 17, and 26-30 stand rejected under 35 U.S.C. § 103(a) as allegedly obvious over Liu and a secondary reference. Specifically, claims 1 and 3 stand rejected as allegedly obvious over Liu in view of Heix. (Office Action, paragraph 9). Claims 1, 13, 14, 16, 17 and 26 stand rejected as allegedly obvious over Liu in view of Braselmann. (Office Action, paragraph 10). Claims 1, 26 and 27 stand rejected as allegedly obvious over Liu in view of Hagmann. (Office Action, paragraph 11). Claims 1 and 28 stand rejected as allegedly obvious over Liu in view of Burge. (Office Action, paragraph 12). Claims 1 and 29 stand rejected as allegedly obvious over Liu in view of Bailey. (Office Action, paragraph 13). Claims 1 and 30 stand rejected as allegedly obvious over Liu in view of Gelfand. (Office Action, paragraph 14).

Liu is cited as above and the secondary references are cited for teaching regulation of rRNA (Heix); an estrogen-related recombinant transcription factor fused to an estrogen regulated activation domain (Braselmann); assays for activation of HSV using VP16 (Hagmann); an algorithm for the prediction of genes in genomic sequences (Burge); expressed sequence tag analysis methods (Bailey); and analysis of cDNA sequences for corresponding genomic sequences (Gelfand).

Because there is no motivation in any of the cited references to use exogenous molecules with known modulatory capabilities to identify genes, Applicants traverse the rejections and supporting remarks.

As noted above, Liu fails to describe or suggest methods in which putative gene sequences are obtained and identified as gene or non-gene. As acknowledged by the Office, Liu relates entirely to modulation of expression of a known reporter gene, where modulation itself is the end goal. In contrast, the claimed methods are directed to a completely different end point, namely the identification of a sequence as gene or non-gene. Moreover, there is no motivation to

combine Liu with any of the secondary references and certainly no combination of Liu and any of the secondary references that would reasonably lead one of skill in the art to the claimed methods. Heix, Braselmann and Hagmann are completely silent as to how one would go about identifying whether any given sequence is in a gene. For their parts, there is absolutely no suggestion or motivation in Burge, Bailey or Gelfand to use an exogenous molecule in combination with gene prediction algorithms or methods to identify genes. Simply put, there is no combination of Liu and any of the secondary references that renders the pending claims obvious. Accordingly, Applicants respectfully request that the rejections be withdrawn.

CONCLUSION

Applicants believe that the claimed subject matter is now in condition for allowance and early notification to that effect is respectfully requested. If any issues remain to be addressed, the Examiner is encouraged to telephone the undersigned.

Respectfully submitted,

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